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Zoonotic Transmission of Waterborne Disease: A Mathematical Model

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Zoonotic transmission of waterborne disease: a mathematical model

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Abstract Waterborne parasites that infect both humans and animals are common causes of diarrheal illness, but the relative importance of transmission between humans and animals and vice versa remains poorly understood. Transmission of infection from animals to humans via environmental reservoirs, such as water sources, has attracted attention as a potential source of endemic and epidemic infections, but existing mathematical models of waterborne disease transmission have limitations for studying this phenomenon, as they only consider contamination of environmental reservoirs by humans. This paper develops a mathematical model that represents the transmission of waterborne parasites within and between both animal and human populations. It also improves upon existing models by including animal contamination of water sources explicitly. Linear stability analysis and simulation results, using realistic parameter values to describe *Giardia* transmission in rural Australia, show that endemic infection of an animal host with zoonotic protozoa can

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result in endemic infection in human hosts, even in the absence of person-to-person transmission. These results imply that zoonotic transmission via environmental reservoirs is important.

Keywords Mathematical model · Protozoa · Zoonoses · Waterborne disease

Mathematics Subject Classification (2000) 92D30 · 92D40 · 92B05

1 Introduction

Waterborne protozoa that infect both humans and animals, including *Cryptosporidium* and *Giardia* species, are significant public-health problems, with about 58 million cases of childhood diarrhea worldwide due to protozoan infection annually (Savioli et al, 2006). The exact role of zoonotic (animal to human) transmission in the epidemiology of these infections is still poorly understood, with *Giardia* and *Cryptosporidium* both classed as neglected tropical diseases because of the lack of research attention they have received relative to their epidemiological importance (Kline et al, 2013). Correlational studies have attempted to elucidate the importance of direct zoonotic transmission (Fayer et al, 2010, 2007, 2006; Swaffer et al, 2014) but have not definitively proven the relative importance of environmentally mediated zoonotic transmission, where parasites enter a water source from an animal host's faeces and are then ingested by humans, compared to direct person-to-person or animal-to-human transmission. For the two most common waterborne pathogenic protozoa, *Cryptosporidium* and *Giardia*, transmission from person-to-person (either directly or via the environment) is thought to be more important than zoonotic transmission (Chalmers et al, 2011; Nasser et al, 2012), but this may not be true for some species of *Cryptosporidium*, particular *Cryptosporidium parvum* (Hunter and Thompson, 2005). Whilst a number of mathematical models exist of the transmission of water-borne infections via environmental reservoirs (Chick et al, 2002; Eisenberg et al, 2002, 2004; Li et al, 2009; Tuite et al, 2011), these models have humans as the source of pathogens in the environmental reservoir and are therefore inappropriate for studying the importance of environmentally mediated zoonotic transmission. In this paper, a more complex model, which instead incorporates animals as the source of pathogens in the environmental reservoir, is devised. The model is analysed mathematically, showing that the importance of environmentally mediated zoonotic transmission may be underestimated; in fact, endemic infection with waterborne protozoa in humans may be completely explained by this transmission route. The model is then applied to the study of waterborne protozoan disease in rural Australia. Australia appears to be particularly vulnerable to outbreaks of waterborne disease; of 199 documented waterborne disease outbreaks between 2004 and 2010, 46.5% occurred in Australia (Baldursson and Karanis, 2011). From 2003 to 2009 acute *Cryptosporidium* infections in the Australian state of New South Wales increased almost tenfold (from 2.7 to 19.8 cases per 100,000 people) (Waldron et al, 2011) and *Giardia* cases increased by approximately 30% Australia-wide over a similar period (Kirk et al, 2014). *Giardia*

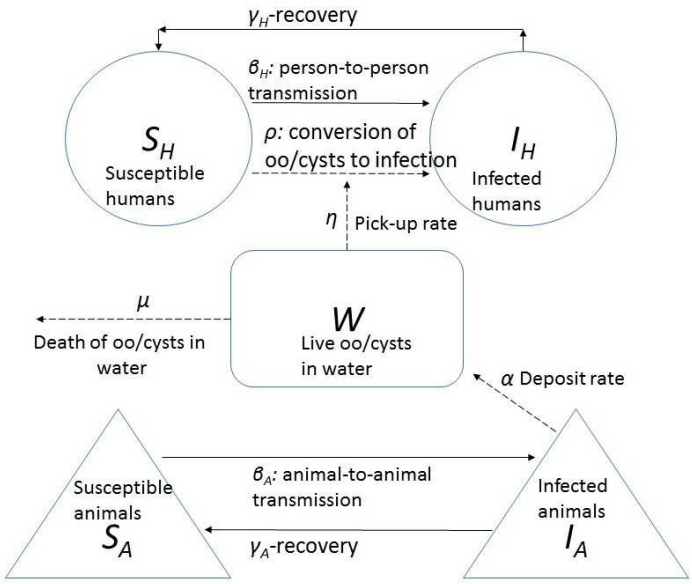

Fig. 1 Graphical representation of the process of environmentally-mediated transmission of protozoan infections from animals to humans, as described by the system of equations (6). The term oo/cyst is used to denote the free living life stage of a protozoa.

infection is, however, more severe than *Cryptosporidium* infection, resulting in the loss of three times as many disability adjusted life years annually (Gibney et al, 2014). For this reason, this paper uses the model to study *Giardia* transmission, though it can easily be adapted to the study of *Cryptosporidium* (Thompson and Smith, 2011). Using realistic parameter values, we find that environmentally mediated transmission via an endemically infected host could drive infection in the human population. These results suggest zoonotic transmission of *Giardia* could be more important than commonly thought and support the conclusions drawn from mathematical analysis of our model. The importance of environmentally mediated zoonotic transmission of waterborne protozoa should be further studied.

2 Mathematical model

The susceptible–infected–susceptible (SIS) framework, where infected hosts become susceptible once again after recovering from infection (Anderson and May, 1991), formed the basis of our model of rural *Giardia* infection, as the best fit to the currently poorly understood epidemiology of many protozoan parasites. Factors supporting use of the SIS framework are that it is apparent that the symptomatic state (assumed to be infectious) can reoccur within the same individual and that any immunity conferred is at best partial (Casman

et al, 2000; Esch and Petersen, 2013; Newman et al, 2001). The existence of partial or temporary immunity might support using a $SIRS$ model that includes a recovered state, but unfortunately it is unclear how the recovered state relates to asymptomatic carriage of protozoan infections, which may be both protective and potentially infectious (Quilliam et al, 2013; Tysnes et al, 2014). These factors, and the undeniably endemic nature of protozoan infection in some communities (certainly for children) (Asher et al, 2014; Desai et al, 2012), support the parsimonious choice of the simplest possible model for endemic infections: the SIS model (Clancy and Mendy, 2011). From this basic framework, a deterministic compartmental model, represented schematically in Figure 1, was developed to include three types of state entities: 1) humans, divided into susceptible (S_H) and infectious (not necessarily symptomatic) (I_H) states; 2) animals, divided into susceptible (S_A) and infectious (not necessarily symptomatic) (I_A) states, and live pathogen in water (W). The term oo/cyst is used to describe the free-living life stage of a protozoan pathogen in water; the free-living stage of the two most common pathogens, *Cryptopsoridium* and *Giardia*, is an oocyst or cyst, respectively. The dynamics of infection in the animal population as a function of time are modelled using the SIS equations

$$\begin{aligned} \dot{S}_A &= (-\beta_A S_A + \gamma_A) I_A \\ \dot{I}_A &= (\beta_A S_A - \gamma_A) I_A, \end{aligned} \tag{1}$$

where β_A is the transmission rate per animal per unit time and γ_A the recovery rate per unit time. For the remainder of this paper, the unit of time is assumed to be one day, the shortest increment of time that would be useful in most practical applications of this model. Assuming that the host animal population is of constant size $N_A = S_A + I_A$, (1) can be reduced to the single logistic equation

$$\dot{I}_A = (\beta_A N_A - \gamma_A) I_A - \beta_A I_A^2. \tag{2}$$

The change in the number of live oo/cysts per litre of water (W = oo/cysts per litre), as a function of time, is given by the ordinary differential equation

$$\dot{W} = \alpha I_A - \eta W (S_H + I_H) - \mu W. \tag{3}$$

In (3), μ is the rate per unit time at which oo/cysts are eliminated from water by naturally dying; α is the oo/cysts per animal per litre per unit time rate at which infected animals contaminate water; and η is the rate per person per unit time at which humans ingest cysts by consuming water.

The change in the number of infected people as a function of time is modelled using the SIS equations

$$\begin{aligned} \dot{S}_H &= -\rho\eta W S_H - \beta_H S_H I_H + \gamma_H I_H \\ \dot{I}_H &= \rho\eta W S_H + \beta_H S_H I_H - \gamma_H I_H, \end{aligned} \tag{4}$$

where β_H is the per person per unit time and γ_H the per unit time rate at which susceptible persons acquire infection from other individuals and recover from infection. The parameter ρ is the rate at which individuals who have ingested oo/cysts become infectious, with units of persons per oo/cysts per litre. Let the human population be of constant size $N_H = S_H + I_H$, such that (4) can be rewritten as the single extended logistic equation

$$\dot{I}_H = \rho\eta W(N_H - I_H) + (\beta_H N_H - \gamma_H)I_H - \beta_H I_H^2. \tag{5}$$

The three equations (2), (3) and (5) together comprise the system of equations

$$\begin{aligned}
\dot{I}_A &= (\beta_A N_A - \gamma_A)I_A - \beta_A I_A^2 \\
\dot{W} &= \alpha I_A - \eta W N_H - \mu W \\
\dot{I}_H &= \rho\eta W(N_H - I_H) + (\beta_H N_H - \gamma_H)I_H - \beta_H I_H^2,
\end{aligned} \tag{6}$$

which describes the environmentally mediated transmission of protozoan infection from animals to humans, as shown schematically in Fig. 1.

The system (6) has three equilibrium points: the disease-free equilibrium $(0, 0, 0)$, endemic disease in the human population as a result of human-to-human transmission $(0, 0, N_H - \gamma_H/\beta_H)$, and a third equilibrium with endemic disease in both the human and animal populations, mediated by waterborne transmission. The solution at this third equilibrium point is given by the vector

$$\begin{pmatrix} \hat{I}_A \\ \hat{W} \\ \hat{I}_H \end{pmatrix} = \begin{pmatrix} N_A - \dfrac{\gamma_A}{\beta_A} \\ \dfrac{\alpha N_A - \dfrac{\alpha\gamma_A}{\beta_A}}{\eta N_H + \mu} \\ \dfrac{-B \pm \sqrt{B^2 - 4AC}}{2A} \end{pmatrix}, \tag{7}$$

where

$$\begin{pmatrix} A \\ B \\ C \end{pmatrix} = \begin{pmatrix} \beta_A\beta_H(\eta N_H + \mu) \\ \rho\eta\alpha\gamma_A\left(\dfrac{\beta_A N_A}{\gamma_A} - 1\right) + \beta_A\gamma_H(\eta N_H + \mu)\left(1 - \dfrac{\beta_H N_H}{\gamma_H}\right) \\ \rho\eta\alpha\gamma_A N_H\left(1 - \dfrac{\beta_A N_A}{\gamma_A}\right) \end{pmatrix}. \tag{8}$$

The three eigenvalues (λ_i) of the Jacobian matrix of (6) evaluated at the

equilibrium point (7) are

$$\begin{pmatrix}\lambda_1\\ \lambda_2\\ \lambda_3\end{pmatrix} = \begin{pmatrix} \gamma_A\left(1-\dfrac{\beta_A N_A}{\gamma_A}\right) \\ -\eta N_H-\mu \\ \dfrac{-\rho\eta\alpha\gamma_A\left(\dfrac{\beta_A N_A}{\gamma_A}-1\right)}{\beta_A(\eta N_H+\mu)}+\gamma_H\left(\dfrac{\beta_H N_H}{\gamma_H}-1\right)-2\beta_H\hat{I}_H \end{pmatrix}. \quad (9)$$

Under the assumption that realistic values for all parameters are all greater than or equal to zero, $\lambda_1 < 0$ when $R_{0A} = \beta_A N_A/\gamma_A > 1$, and $\lambda_2 < 0$ always. Define the basic reproduction number R_{0i} as the number of new infections arising in a population of species i; commonly, when this number exceeds one, an epidemic can commence in host i (Anderson and May, 1991; Keeling and Rohani, 2007). Were the normal dynamics of the SIS model to apply, the existence of a stable equilibrium with disease in the animal and human populations would require that $R_{0i} > 1$ for both humans and animals. Whilst it is clear that $R_{0A} > 1$ is required for stability, solving the inequality $\lambda_3 < 0$ shows that the behaviour of the model is different to the standard SIS model, as endemic disease in the animal population drives infection in the human population even while $R_{0H} < 1$. Given $\beta_A N_A/\gamma_A > 1$ (since $\lambda_1 < 0$) and assuming that only positive values of $\hat{I}_H$ are meaningful, the first and third terms in λ_3 are negative. When $R_{0H} = \beta_H N_H/\gamma_H < 1$, the second term in λ_3 is also negative, and hence $\lambda_3 < 0$ overall. Therefore a stable equilibrium with disease in both the animal and human population exists only if $R_{0A} > 1$ and $R_{0H} < 1$.

For completeness, we will discuss the stability of the first two equilibrium points. The three eigenvalues of the Jacobian matrix evaluated at the disease-free equilibrium and the second equilibrium point, corresponding to endemic disease in the human population as a result of human-to-human transmission, can be shown to be

$$\begin{pmatrix} \gamma_A\left(\dfrac{\beta_A N_A}{\gamma_A}-1\right) \\ -\eta N_H-\mu \\ \gamma_H\left(\dfrac{\beta_H N_H}{\gamma_H}-1\right) \end{pmatrix} \text{and} \begin{pmatrix} \gamma_A\left(\dfrac{\beta_A N_A}{\gamma_A}-1\right) \\ -\eta N_H-\mu \\ \gamma_H\left(1-\dfrac{\beta_H N_H}{\gamma_H}\right) \end{pmatrix}, \quad (10)$$

respectively. As stated before, we should assume only positive parameter values as meaningful. By examining the eigenvalues (10), the disease-free point is stable (all three eigenvalues are less than zero) if both R_{0A} and R_{0H} are less than one. On the other hand, the second equilibrium point is stable when $R_{0A} < 1$ and $R_{0H} > 1$.

Summarising the results presented here, if $R_{0i} > 1$ for either humans or animals, the disease-free state is unstable. Where $R_{0H} > 1$ and $R_{0A} < 1$, the system tends towards the second equilibrium point with disease in the human population only; if $R_{0A} > 1$ but $R_{0H} < 1$, the system tends towards the third equilibrium point, where endemic disease in the animal population is sufficient to cause endemic disease in the human population also.

3 Application of the model to the case of *Giardia* transmission from possums to humans

Numerical methods were employed to demonstrate the implications of Section 2 for understanding the phenomenon of high *Giardia* prevalence in rural Australia. In Australia, as in other parts of the world, pockets of symptomatic *Giardia* infection (giardisis) occur in rural locations (Fletcher et al, 2014; Lal et al, 2013). A number of explanations have been proposed for the clustering of *Giardia* infection in rural areas. Larger populations of agricultural livestock and wild animals in rural areas suggest that increased zoonotic transmission of *Giardia* infection in rural areas may be important (Borchard et al, 2010), but the epidemiological evidence for any direct transmission from either agricultural or wild animals to humans remains weak (Caccío et al, 2005; Hunter and Thompson, 2005). A more likely explanation for the crowding of *Giardia* infection in rural areas is the higher use of alternative water sources such as rain or bore water (Fletcher et al, 2014). One author estimates that as high as 82% of rural households in rural New South Wales, Australia, rely on rainwater tanks for household drinking water (Lye, 2002). Rainwater tanks and other alternative water sources are associated with many outbreaks of waterborne disease in Australia (Dale et al, 2010) and often become contaminated with *Giardia* cysts shed in animal faeces (Ahmed et al, 2012). Under this hypothesis, zoonotic transmission is environmentally mediated rather than due to direct contact between humans and animals. Bird and possum[1] faeces are possible sources of *Giardia* contamination of rainwater tanks (Ahmed et al, 2012). Mice and rats are other mammals known to carry *Giardia* (McKenna, 2009) and also have the potential to faecally contaminate rainwater (Abbasi and Abbasi, 2011). Of these hosts, possum faeces most commonly contain *Giardia* cysts ($\sim 30\%$) (Ahmed et al, 2012), so possums were chosen to be the example animal host in these examples. Two examples are used in this section to demonstrate that both the second and third equilibrium solutions of the model (6) can be fitted to the high target prevalence of *Giardia* in rural Australian people. The target prevalences of interest were the proportions of infectious humans and possums. A person or animal was considered infectious if their faeces contained *Giardia* cysts; they did not have to be symptomatic in terms of presenting with diarrhea. There are reasonable estimates of the

[1] Possums are native Australian marsupials, here assumed to be of *Trichosurus vulpecula* species.

proportion of human and possum faeces containing cysts: 7.6% (Feng and Xiao, 2011; Lasek-Nesselquist et al, 2009; Read et al, 2002) and 30% (Ahmed et al, 2012), respectively. Given constant population sizes $N_H = 1000$ and $N_A = 500$, at equilibrium the numbers of infectious humans and possums are 76 and 150. Using these values as the target prevalence values, the second and third equilibrium points of (6) are $(0, 0, 76)$ and $(150, 150/(\alpha(-\eta N_H - \mu)), 76)$. It is apparent that fitting (6) to the second equilibrium point depends only on optimising the parameters of the third equation for disease in the human population, which is equivalent to (5). Considering the third equilibrium point $(150, 150/(\alpha(-\eta 1000 - \mu)), 76)$, observe **that,** because the target prevalence of infection in the possum population and the size of the human population are known, fitting the model can be reduced to the problem of optimising the parameters α, η and μ. Substituting these equilibrium values into (6), observe that each of these parameters to be optimised, plus the final unknown parameter ρ, appears in the third equation — for disease in the human population. Thus the problem of fitting the model to the third equilibrium point can also be addressed by analysing the third equation in (6) only, equivalent to (5).

Bifurcation analysis was used to find the optimal value of $R_{0H} > 1$ by solving (5) given the constraint $\hat{I}_H = 76$ and setting the values of all parameters other than β_H and γ_H to zero. In the deterministic SIS model (5), the removal rate, $\gamma_H/\beta_H N_H$, is equal to $1/R_{0H}$, or equivalently, to the proportion susceptible at endemic equilibrium in homogeneously mixed populations (Anderson and May, 1991; Hethcote, 2000). Therefore a plot of increasing values of the bifurcation parameter R_{0H} can be used to determine the point at which the desired prevalence $(1 - 1/R_{0H})$ is attained.[2] Values of R_{0H} ranging from 1.07687–1.0881 produced the target prevalence of 7.6 (± 0.5)% in the human population (see Fig. 2).

To fit the model to the third equilibrium point, deterministic optimisation methods were used to solve the following non-linear programming problem.

$$\begin{aligned} \text{Minimize:} \quad & 0\alpha + 0\eta + 0\mu + 0\rho \qquad (11)\\ \text{Subject to:} \quad & \rho\eta \left(\frac{\hat{I}_A}{\alpha(\eta N_H + \mu)} \right) \left[N_H - \hat{I}_H \right] + N_H \beta_H \hat{I}_H - \gamma_H \hat{I}_H - \beta_H I_H^2 = 0,\\ & \hat{I}_A = 150, \hat{I}_H = 76,\\ & \alpha, \eta, \rho > 0,\ \mu \geq 0. \end{aligned}$$

By setting the objective function equal to zero, as defined in (11), we cast this problem as a feasibility problem rather than a strict optimisation problem.

[2] This approach was used because of the lack of reliable estimates of γ_H and β_H in the literature. Estimates of the duration of *G. lamblia* infection in humans only describe the duration of symptoms (Gibney et al, 2014; Rendtorff, 1954; Robertson et al, 2010), not infectiousness as defined in this paper, and vary substantially from 2–60 days (Gibney et al, 2014; Nash et al, 1987; Nygård et al, 2006).

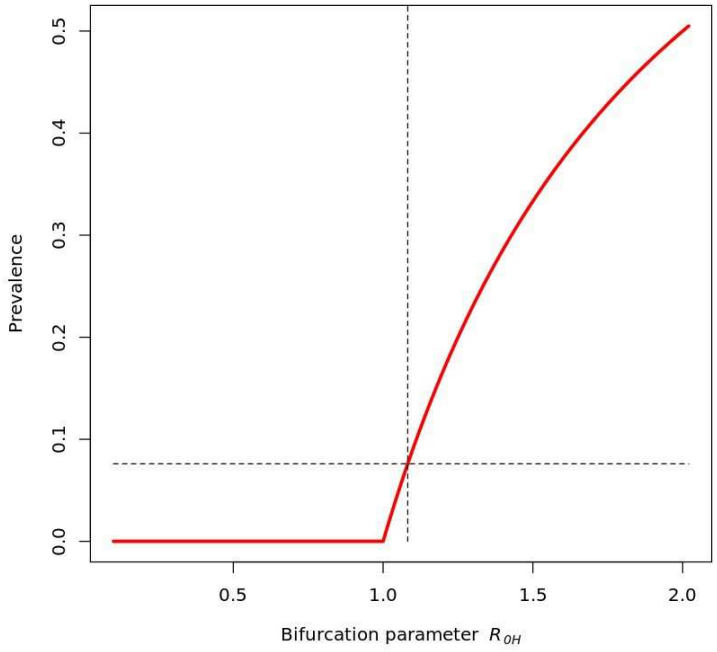

Fig. 2 Bifurcation plot showing that the target *Giardia* prevalence of 7.6% (Feng and Xiao, 2011; Lasek-Nesselquist et al, 2009; Read et al, 2002) is attained in the human population with an R_{0H} value of 1.082.

Table 1 Parameter values and constraints used in optimising the parameters of (5) given $\hat{I}_H = 76$, $\hat{I}_A = 150$ and $\hat{W} = 150/(\alpha(-\eta 1000 - \mu))$.

Parameter	Initial value	Final value	Constraint
Rate of conversion of ingested cysts to infection ρ (persons per cysts per litre)	0.02 (Rose et al, 1991)	0.02	$\rho > 0$
Deposit rate α (cysts per litre per animal per day)	0.01	0.49	$\alpha > 0$
Pick-up rate η (per person per day)	0.01	3.4×10^{-4}	$\eta > 0$
Decay rate in the environment μ (per day)	0.36 (Bingham et al, 1979; DeRegnier et al, 1989)	0.03	$\mu \geq 0$

This approach is appropriate because there is no established notion of an optimal parameter set for this problem, but there are **well-established** biological constraints limiting solutions to a feasible region. Additionally, problem (11) has non-linear constraints, which **makes** it difficult to solve exactly. By using our **approach,** all solutions to the objective function will equal zero and be equally optimal, making the problem easy to solve, but biological realism is preserved by the fact that not all of these solutions are feasible given the constraints. In general, recasting such optimisation problems in this way is an efficient option as feasible solutions can be readily identified by sophisticated optimisation tools, such as those in **Matlab.** To solve (11) given the constraints, we utilised an algorithm that checks first-order necessary conditions for an optimiser, namely, the built-in `fmincon` function that exists within the **Matlab** Optimization Toolbox. The formulation of the problem assumed constant values of all other parameters and variables. Values of β_H and γ_H were chosen that gave a value of the bifurcation parameter R_{0H} close to zero (0.01) to convincingly demonstrate that high *Giardia* prevalence in the human population could be driven solely by environmentally mediated transmission from the possum population. There are no estimates of the transmissibility of *Giardia* or the duration of infectiousness in possums, so bifurcation analysis was used to determine the optimal value of R_{0A} (as described above for the human population) and appropriate values of β_A and γ_A were inferred from this. Values of R_{0A} between 1.418 and 1.439 produced the target prevalence of 30.0 ($\pm$0.5)%. Initial values for all other parameters are given in Table 1. Initial values of α and η were set close to zero in the absence of data. The solution to (11) is given in Table 1. The solution shows that, with realistic values of the parameters α, η, μ and ρ, the target *Giardia* prevalence in the human population can be produced with almost zero person-to-person transmission. This numerical analysis shows the realism of our analytical findings and has important implications for the study of *Giardia* and other zoonotic, waterborne pathogens.

Deterministic sensitivity analysis was conducted by iteratively solving (11) for $\hat{I}_H \in [71, 81]$ (the tolerance region set around the target prevalence above). The parameters η, ρ and μ increased linearly in response to increasing values in $\hat{I}_H$. In contrast, the parameter α decreased linearly. This is depicted **in Figure** 3 below. The parameter variations are shown in Table 2.

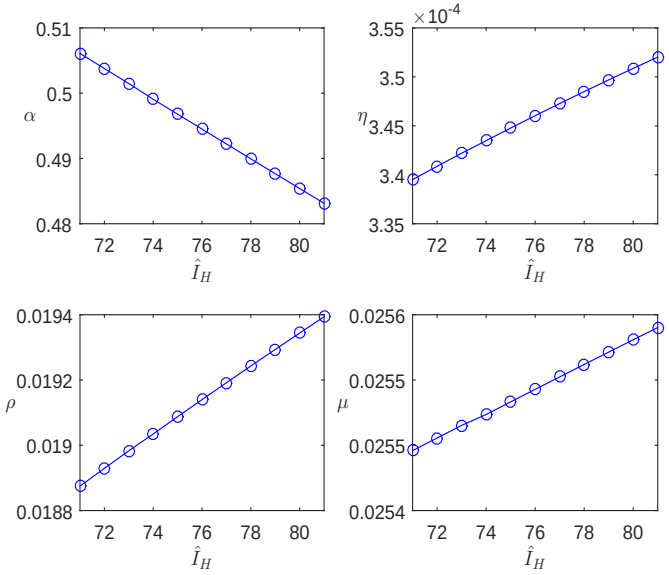

Fig. 3 The variation in parameter values with respect to the change in $\hat{I}_H$.

Table 2 Change in parameter values for changes in the equilibrium number of infectious humans $\hat{I}_H \in [71, 81]$.

Parameter	Range
Rate of conversion of ingested cysts to infection ρ (persons per cysts per litre)	[0.018, 0.019]
Deposit rate α (cysts per litre per animal per day)	[0.483, 0.506]
Pick-up rate η (per person per day)	$[3.4 \times 10^{-4}, 3.5 \times 10^{-4}]$
decay rate in the environment μ (per day)	[0.026, 0.027]

4 Discussion

A number of studies worldwide have suggested land-use as a risk factor for infection with *Giardia* (Borchard et al, 2010; Lal et al, 2013). The importance of this pathogen seems to be growing in Australia, with the incidence of symptomatic infections increasing by 30% Australia-wide in the period from 2000 to 2010 (from 2,600 to 3,700 cases) (Kirk et al, 2014). According to some authors, this trend is likely to continue, with increasing use of rainwater and increasing temperatures due to climate change cited as risk factors for waterborne disease (Fletcher et al, 2012). Whilst these factors have been studied in relation to other pathogens such as *Cryptosporidium* (McBride et al, 2014), this is the first paper that explicitly explores one of these factors—rainwater—in relation

to *Giardia* using a mathematical model.

This paper describes a new model that differs in two important ways from previous models of the transmission of waterborne disease via drinking water. Whilst a number of previous models of water-borne infections have environmental reservoirs of the pathogen as the main source of transmission (Chick et al, 2002; Eisenberg et al, 2002, 2004; Li et al, 2009; Tuite et al, 2011), these normally have humans as the source of pathogens in the environmental reservoir. The model presented in this paper has animals as the source of pathogen in the environment; in many scenarios, such as the example given of the contamination of rainwater by possums, this is a more plausible source of pathogen in the environment than human faeces. The model further differs from previous similar models by including a compartmental model of the infection process in the animal host. Linear stability analysis of the model is used to demonstrate that disease in an animal host can drive endemic infection of the human population, even if the basic reproduction number describing the number of people infected by another person (R_{0H}) is less than one. This result supports the hypothesis that environmentally mediated zoonotic transmission is important in *C. parvum* epidemiology (Hunter and Thompson, 2005). This hypothesis is also supported by the effectiveness of measures such as reducing cattle density in reducing the occurrence of *C. parvum* infection (Xiao and Feng, 2008). On the other hand, the result challenges existing assumptions about the epidemiology of another important protozoa, *Giardia*. Some experts consider zoonotic transmission to be less important for *Giardia* than for *C. parvum* (Hunter and Thompson, 2005), suggesting that humans are more likely to infect animals with the parasite rather than vice versa (Thompson and Smith, 2011). Our results, which do not support this latter hypothesis, are obviously related to our choice of model structure; nonetheless, if our model structure is in fact an appropriate representation of the process of environmental transmission of *Giardia*, our findings have the potential to cause us to rethink our attitudes to this parasite.

It is notable that all the feasible parameter values identified during optimisation of the *Giardia* modelling scenario were plausible, given existing empirical estimates. Similarly, the final value of the ρ parameter was identical to the best estimate for this parameter in the microbial risk assessment literature – 0.0198 (95% CI 0.01,0.036) (Rose et al, 1991). Additionally, the variation in ρ remained within these bounds during sensitivity analysis (see Table 2). There is very little empirical information about the parameters α and β, but the final values of both seem plausible. A value of $\alpha = 0.5$ implies that the average infected animal deposits half a cyst into a litre of rain water per unit time but that humans only ingest these cysts at a much lower rate (3.4×10^{-4}); this seems feasible. Therefore the numerical simulations contained in this paper show that the prevalence of just one waterborne pathogen (*Giardia*) in humans can be explained virtually entirely by zoonotic transmission via environmental reservoirs, using realistic parameter values. The extent to

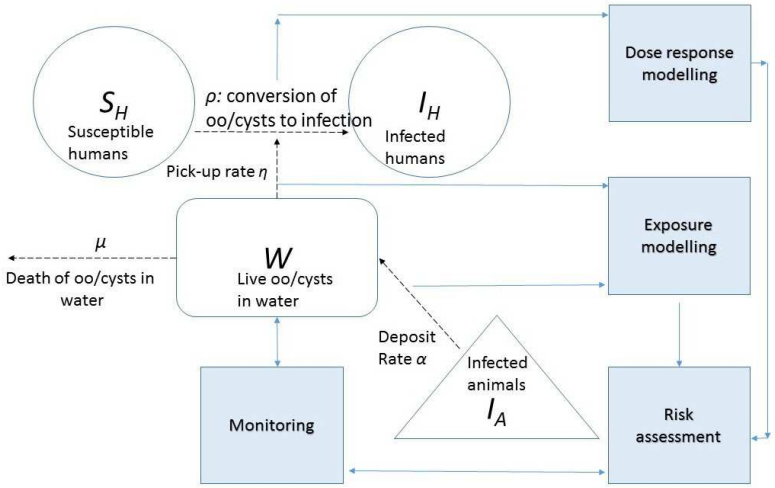

Fig. 4 Schematic showing how relevant processes within the transmission model (from Figure 1) are linked to monitoring and risk assessment activities (blue boxes).

which this is true for similar pathogens, such as *Cryptosporidium*, is an avenue for further research using the model formulated in this paper.

The model presented in this paper has a number of limitations that could be improved upon in future research. Use of the SIS framework is an oversimplification, and future work should extend the model to incorporate at least temporary or partial immunity (Quilliam et al, 2013; Solaymani-Mohammadi and Singer, 2010; Tysnes et al, 2014). Another important avenue of future research is modelling the potential public health impact of different interventions targeting either the pick-up rate η or the deposit rate α, such as water filtration and treatment and the culling of animal hosts. Climatic variables such as rainfall and temperature have the potential to influence a number of parameters in the model, such as the deposit rate and survival of pathogens in the environment (Lal et al, 2013). Including the effect of climate on the pathogen load in the environment would also improve the model and make it more useful for exploring critical issues such as the impact of climate change on the spread of zoonotic waterborne disease (McBride et al, 2014).

The clear connection between our model and parameters used in risk assessment, such as pathogen concentration in water, pick-up rates and deposit rates, indicate the potential implications of the work contained in this paper for the field of quantitative microbial risk assessment (QMRA). QMRA is the most important tool for quantifying waterborne disease risks in general, and forms the basis of microbial risk management in major water-quality guidelines, including the Australian Guidelines for Water Recycling (NRMMC et

al. 2006), the WHO Guidelines for the Safe Use of Wastewater, Excreta and Greywater (WHO 2006) and the WHO's (2011) Guidelines for Drinking-water Quality. Briefly, QMRA is a four-step process comprising (i) hazard identification, (ii) exposure assessment, (iii) dose-response modelling, and (iv) risk characterisation. Practitioners and researchers utilising each of these processes will be particularly interested in insights our model provides about likely values of particular parameters, as shown in Figure 4. Hazard identification involves determining the pathogen(s) of concern; exposure assessment comprises defining the exposure pathway so the dose of the pathogen(s) to which a person is exposed can be determined; dose-response modelling defines the probability of infection as a function of this dose; and the final step, risk characterisation, brings all this together to arrive at an estimate of the probability of an adverse outcome, typically infection or illness. Many QMRA models have been constructed for waterborne transmission of *Giardia* (Westrell et al, 2004; Mota et al, 2009; Razzolini et al, 2011; McBride et al, 2013; Xiao et al, 2013), but these models, like QMRA models generally, are limited by the fact that they ignore the transmission of infection from person to person, animal to animal and animal to person completely. QMRA and epidemiological models like the one in this paper need not be mutually exclusive areas of research though; rather, QMRA could readily be dovetailed into a modelling framework such as the one presented here. As shown in this paper, an immediate benefit of this type of modelling for QMRA is its ability to test common assumptions. *Giardia*, unlike *Cryptosporidium*, is thought to be characterised by high person-to-person transmission—but the results presented in this paper show that the same prevalence of *Giardia* in the human population can be arrived at through either high person-to-person or environmentally mediated zoonotic transmission. Determining which of these scenarios is most important is a topic for further research, but either scenario obviously has implications for risk assessment using QMRA.

5 Conclusion

Waterborne protozoa, including *Giardia* and *Cryptosporidium*, are common causes of diarrheal illness. These parasites infect both human and animal hosts, but the relative importance of transmission between humans and animals and vice versa remains poorly understood, as does the role of environmental reservoirs in this process. Existing mathematical models of water-borne disease transmission between animals and humans via environmental reservoirs, such as water sources, have limitations, as they only consider contamination of environmental reservoirs by humans. This paper described a mathematical model that represents the transmission of waterborne parasites within and between both animal and human populations. This model improves upon existing models by including animal contamination of water sources explicitly. Linear stability analysis and simulation results, using realistic parameter values to

describe *Giardia* transmission in rural Australia, show that endemic infection of an animal host with zoonotic protozoa can result in endemic infection in human hosts, even in the absence of person-to-person transmission. These results suggest that the importance of zoonotic transmission via environmental reservoirs may be underestimated.

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